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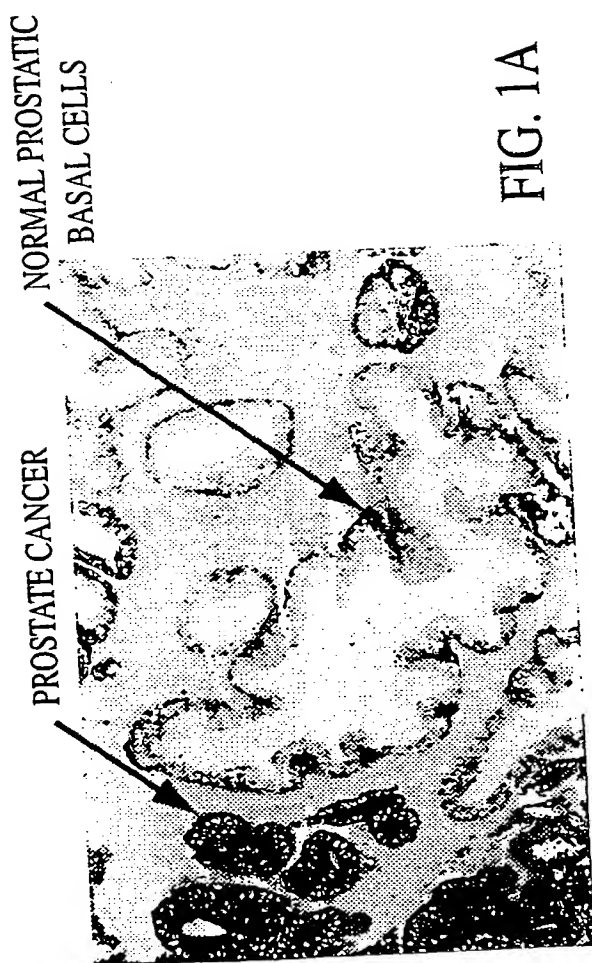


FIG. 1A

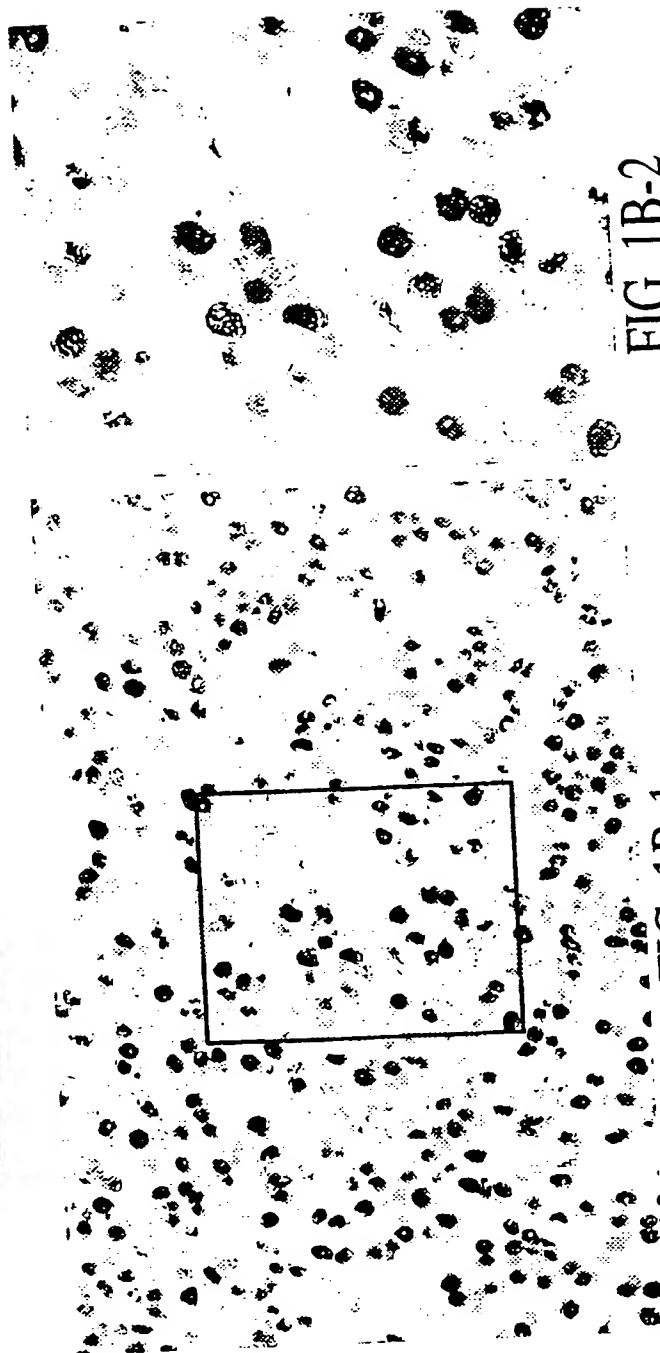


FIG. 1B-2

**FIG. 1B-1**

1 AAGCTTTCCT GATCTCTAAA TCAAGGTCAG CTCCCTAAGC TCTTGGCTCC  
 51 CGTACTGAAA CTTTTTCTTA TGTAACCTCTC ATAAACACAT AGCATAATGT  
 101 TTTGCATGTT TTTCTTCCCT ATCAGTTGCA AGTTCAGCA GAGCTGATAT  
 151 ATTTTCATTT CATTCGCTAC TATAGCCCTA GAGCCTGACA TAGTTTCTGG  
 201 CTGTGAATGC TCAATAAATA TTTGTTTAAT TGAGTAGAAA CATAAAGTAT  
 251 CTATTTTCATT GAAGGAAAGA ATAATTAGCT ACATTTTTCT TTTTCTTGCC  
 301 TTAATATTTG AGGAATTTGC TTATATGTCA TAATAAAAAA GTTAAAGCCT  
 351 TATACATTAT ACTAAGGAAT TTGGACATTA AATTCAAGCT AGCCTTTCTA  
 401 TAAACAAAAT ACTGAATTTT TGTCCCTAAA TTTGTTCTT CCCTATTCTT  
 451 CCCCATTGAG ATGACACCAA ATCCCTCTAG CTGCTCAAAC CAAGTACCCG  
 501 TATGTTATTC TTAATTATCT CTTTACCTTG CTTCATAT GCAATTTGTT  
 551 AACAAAGTCAT CTTCAAGTCTG TATCCATTAT TCTCCCTTTC CAGACCACCA  
 601 ACATGTCTTG ACTATACTGC TACAATAGCC TCCCAACTCT TGTCTACTT  
 651 AAAATTCATT GTAAAAAATC AGTCTTGGCC GGGCACGGTG GCTCACACCT  
 701 ATAATCCCAG CACTTTGGGA GTCCCAGGCG GGC GGTCAC GAGGTCAAGA  
 751 GATGGAGACC ATCATGGCCA ACATGGTGAA ACCCTGTCTC TACTATAAAT  
 801 ACAAAAAAAT TATCTGGGTG TGGTGGCACA TGCCTGTAAT CCCAACTACT  
 851 AGGGAGGCTG AGGCAGGAGA ATCGCTTGAA CCTGGGAGGC GGAGGTTGCA  
 901 GTGAGCCGAG ATCGCACCAT TGCACTCCAG CCTGGCAACA GAGCGAGACT  
 951 CCATCCCCAA ACAAAACAAA ACAAAACCAT GTAAAACATG TCTGTAAAAC  
 1,001 ATGTCAGATT TCGTGTTTCA AAGTCTTACA TGTCTTTTCA TTATGCTAAG  
 1,051 ATAAAACCCA AATGCATTTT CTTGGTTTCT AAAGCCAAGA AAATAAGAGT  
 1,101 TGCTTTCAGC AACCTTGTTT CTTCCGCCAT GCTTTTCCCT AGCTCACTCT  
 1,151 TTTTAGGCAA GTCGACCTGA TTTTCTTTCT GTTAGTCTGT TTCTGCCTCG  
 1,201 TGGTCTGGCT TTCTTTCTGT TAGTCTGTTT CCACCTCGTG GTCTTGGTCC  
 1,251 TGGCTCTTCA TTCTGCCTGG AATGCTCTCC ACTCCAGATC CTTACTAGAT  
 1,301 CTTAGCTCAG TCATCACCCCT CGCAGGAAGA TCTTCCAACC ATTCACCTGC  
 1,351 ATACACCTAT GGCTGCTCCC TAGAGAACAT CATTCTGTTT TCTTCACTTC  
 1,401 CTAGCACTTA CTGCTTTCTG AAATTATCTA CTTTGATTGT TTATTTCTTT  
 1,451 CTTTACTCTT ACTAGGATAC CTGGGTCATT AAAGGAGGGA TATTTCTCTC  
 1,501 TTATTTACTG TTATAAACTT AATGCTTAGG CTGTAGAAGT TATACAATAT  
 1,551 TTGAAGAATA AATCGTTAAA TGTATAACAT TTTTGAAGAA AGATAATTGT

FIG. 2

FIG. 2 - Continued

1,601 GGGATCCATT TAGTTTGCAA ACATTTGATC TGTGTGTTAG ACAGAAGGCC  
 1,651 ATGGTAAAGG ACAAAGACAT ATTTTATAGG ACTGTACCCT GAAAAATAAA  
 1,701 TAAACTTGAA CCAGTTATAC AAGACTTATG TGCAGGAAAC AGGTACCAGT  
 1,751 TATATTTAGA AATGGTAAAT CACCTTCTAA GCATAACTCA GAGCACAATA  
 1,801 TATTAGAGGG TAGAGAGAGA AGTGCCTCTT AGATATTGGT AATCATATTA  
 1,851 GGA CTGACGC CATCCTTGAT TTTTCTTCTG GGAAACAGCT CAAAATGACT  
 1,901 ATTTAATGTT TACAATGATA TCTTGCATCT TGCCAGTAAA TAATATAATA  
 1,951 GACACTAGGA ATCCAAATTG TAAGATGAAC AAGTCTTTAT AGAGGGGAGAG  
 2,001 CCAAATACAC AATAAATAAC ACAAGGTGGT AAATGCAGTA ATACAAACAT  
 2,051 ACATACCATG CATAGGAGTG CAGAGAAGGT GTGCTTCTCC GAATGCAGTC  
 2,101 ACCCAGAAAG TCCTTCTGTA GAAAGGGATA TCTTAAATGG TGCTTAAAGG  
 2,151 AAAAGTAACC AAAGGCAACT AAAGATTGCA AGGAGGTCCC AGGAAAAAGC  
 2,201 AAAAGAACCA AAGGTACATA GGCACAAAAG TAGCCTGCCT TCCTGGGAAC  
 2,251 TTCCAATAGT TTGCTGGAGC ACACAGTTAG AAGTACTGTG CCATGGGAGC  
 2,301 AAAGACTGAA GACATATGCA GGTTC AAGGG CACAGAGCCC CATATATGTC  
 2,351 ATGATAAGAT ATTGGGAAGC CACTGGGGAG CTACTGAAAC TTTAAGCAGG  
 2,401 GAAATAAAAT TGTCATATCT ACACCTTAGA AATTTGATTT TTTTCTCTTC  
 2,451 TTTTATCTTC TCTTCTCCTC TCTTCTCTCT CTCTCTCTCT CTCTCTCTCT  
 2,501 GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GACAGAGTCC TGCTCTGTCA  
 2,551 CCCAGGCTGG AGTGTAGTGG AGTGATCTCC GCTTACTGCA GTCTCTGCCT  
 2,601 CTCAAGCGAT TCCCTGCCTC AGCCTCCCGA GTAGCTGGGA TTACAGGCGG  
 2,651 GCTCTACAAC AGCTGGCTAA CTTTTGTATT TTTTGGTAAC AACCAGGTTT  
 2,701 TACCATGTTG GCCAGGCTGG TCTTGAATC CTGACCTCAG GTGATCTGCC  
 2,751 TGCCTTGGCT TTCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCCTGCCT  
 2,801 GGTGTAGAAG TTTGATTTTG ATGTCAGTGT GG TAGATGAA TTTGTGGGAA  
 2,851 GCAAAACAAG ATAGAGTTCA ATGACAGTGA AAAGTTTATT GTATAAGCTA  
 2,901 TATAAAAGAA AATGTTGAAG GTTTGAAATC CATTAGTGGC AGTAAGGGTG  
 2,951 TACAGAACGA AACTATTTGA GAAGTACACA AGGCAAGTCT TACTTTCAAG  
 3,001 GCAGTTTATG TAAGCTCATT CAATTGTCTC AGTGTTCTTG CTATGTGTGG  
 3,051 GTTATAGGAT TTGGAACATA TGATCAATCT GAGCACACAT CAGTAAACTG  
 3,101 AATAGGATTA TTAAAATCCA CAAGCATTTT ACTAGTGGAA TCTGTGATAT  
 3,151 TTTCTAGCTA CTCTTGCTTG TTTTATTTGA ATCTTTTGCT CATATCCTAT  
 3,201 AGTAAAGATT TCAGGAAATA TATTTTTATT TGCCTAGAAT TTTAGCCTTT

FIG. 2 - Continued

3,251 TAGTTTTTTG AATCTATTGC TCATATTCTT ATAGTAAGAG TTTCAGGGAA  
 3,301 TGTATTTCTA TTTGTCTGGA ATTTTAGCCT TTCAGGTTTT TGAGCCCCTC  
 3,351 TTTTGCTTAT GGGACATAGT ATGAGACAAG ATGAAATGAT ACTTCTATTC  
 3,401 CCAATTCACT GATGGGGAAA ATGAAGCAAA AAATGTTATT CACTCAAGGC  
 3,451 TTCTGCCATG TTTCCTGGTG GAATTACGGC TCAGACACAA ATTTCCCTAAT  
 3,501 GCCTGTGCTG CTAACCTCTC AATAGAACAC TATATTAATT TATCTTCTTC  
 3,551 CTGAGTGTTT TTCCACAAAT CCCATAGCCT GTGAAAAGAT TGTTTTAGGG  
 3,601 AAATATTATT TTTAATATAG CATATTTTGT CAATGTGGGA CATAGGACTA  
 3,651 GTACCTGCTG AAAACCATCT CATGATCCTT GTGTAAGAAC TAATTCACAC  
 3,701 TAGAAATACT ATTTTCCTTG CTCATTAAAA ACATAAATGT CTCAGAAAGT  
 3,751 AAAAAATTAT TCCTCTCTAA ATAAACATAC ATGCCACTCA AATTTTATTC  
 3,801 CTCTACCACT TGCCGTATCT AAACCTAGTT AGATACTTTG GTTTTAGGTA  
 3,851 TAATCTGACA GAACAGATAC AACCAAGATC ACATTGTGAG TCAGAAGTGG  
 3,901 AAAATTCATA ATTCATGATG ATACCAATAA AAGATAGATT TAGCTTTTTA  
 3,951 CAGGATGTTT TTGGCATTTT ATTCTTTCAT TTGAGGGGAG ATCTCACCAA  
 4,001 AATATGTCTT TCATGGTTCA TTGTGTTATT TAATTTCTGT GATGCATATT  
 4,051 CTCAGGTTAC TTTAAACCTA GTCTATAGAT TCAAAGATAT CCCGTGTCAG  
 4,101 GTCTCTAAAA GTAAAAAGAA AAATGGGTAC TTGTGAAGGC TGATTCACAG  
 4,151 TAAGTAGTGT AGAGGGGAGT GCCTTGTGTA TTCACAAATT ATCAACGTGA  
 4,201 GCATCAGATA AGATTTTCTT TAGTCACACA CACCTACCTT CTTACTAGGA  
 4,251 AGATCCATAT ACTTGAATAA TTGTTCTGCT TGACCCAGGT TACTTATCAG  
 4,301 TCCCTTTATT ATAATATTTG TAAATATTGG GGCTCGAGAA CCGAGCGGAG  
 4,351 CTGGTTGAGT CTTCAAAGTC CTAAACGTG CGGCCGTGGG TTCGAGGTTT  
 4,401 ATTGATTGAA TTCGGCTGGC ACGAGAGCCT CTGCAGACAG AGAGCGCGAG  
 4,451 AGATGGAGAT GGGCAGACGG ATTCATTCAG AGCTGCGGAA CAGGGCGCCC  
 4,501 TCTGATGTGA AAGAACTTGC CCTGGACAAC AGTCGGTCGA ATGAAGGCAA  
 4,551 ACTCGAAGCC CTCACAGATG AATTTGAAGA ACTGGAATTC TTAAGTAAAA  
 4,601 TCAACGGAGG CCTCACCTCA ATCTCAGACT TACCAAAGTT AAAGTTGAGA  
 4,651 AAGCTTGAAC TAAGAGTCTC AGGGGGCCTG GAAGTATTGG CAGAAAAGTG  
 4,701 TCCAAACCTC ACGCATCTAT ATTTAAGTGG CAACAAAATT AAAGACCTCA  
 4,751 GCACAATAGA GCCACTGAAA CAGTTAGAAA ACCTCAAGAG CTTAGACCTT  
 4,801 TTCAATTGCG AGGTAACCAA CCTGAACGAC TACGGAGAAA ACGTGTTCAA  
 4,851 GCTTCTCCTG CAACTCACAT ATCTCGACAG CTGTTACTGG GACCACAAGG  
 4,901 AGGCCCCCTTA CTCAGATATT GAGGACCACG TGGAGGGCCT GGATGACGAG

FIG. 2 - Continued

4,951	GAGGAGGGTG	AGCATGAGGA	GGAGTATGAT	GAAGATGCTC	AGGTAGTGGA
5,001	AGATGAGGAG	GGCGAGGAGG	AGGAGGAGGA	AGGTGAAGAG	GAGGACGTGA
5,051	GTGGAGGGGA	CGAGGAGGAT	GAAGAAGGTT	ATAACGATGG	AGAGGTAGAT
5,101	GGCGAGGAAG	ATGAAGAAGA	GCTTGGTGAA	GAAGAAAGGG	GTCAGAAGCG
5,151	AAAATGAGAA	CCTGAAGATG	AGGGAGAAGA	TGATGACTAA	GTAGAATAAC
5,201	CTATTTTGAA	AAATTCCTAT	TGTGATTTGA	CTGTTTTTTAC	CCATATCCCC
5,251	TCCCCCCTCC	AATCCTGCCC	CCTGAAACTT	ACTTTTTTCT	GATTGTAACA
5,301	TTGCTGTGGG	AATGAGACGG	GAAAAGTGTA	CTGGGGGTTG	TGGAGGGAGG
5,351	GAGGGCAGGA	GGCGGTGGAC	TAAAATACTA	TTTTTACTGC	CAAATAAAAT
5,401	AATATTTGTA	AATATTAAC	CGGATACTAG	CTTTGTAGAA	TGATTACTAT
5,451	TAATTATTCT	CTCTCTCTTT	TTATTTTTTTT	ACACATTCTA	TTCTTTTAAG
5,501	TATAGTCCTT	TTAGTCCAAG	GAAAAGGCAC	TACAATCCAC	TTATTAATGC
5,551	TTGCTACTGT	GTTCAAGTAA	AATAAGCTCC	AGGATTTAAC	AAAAAGAGGA
5,601	AAGAAAATAT	TTACAATGAA	AATGTTGCTA	AAAATTTAAA	ACAAATTACA
5,651	GTAAATGTAT	TGTTAAAGCA	AATTCTATTT	TTAAAATTTA	TTAATAAGGA
5,701	AATAATTTGC	TAAAGCAAAT	TTTTGGAAAA	ATAATAATGC	ACTTTATACT
5,751	TGATTTTATT	TATTAAAACA	ATGATTTATA	AGCTT	

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4,357 GAGTCTTCAA AGTCCTAAAA CGTGCGGCCG TGGGTTGAG GTTTATTGAT TGAATTCGGC  
 1 gaattcccaa agtcctaaaa cgcgcggccg tgggttcggg gtttatigat tgaattccgc

4,417 TGGCAGGAGA GCCTCTGCAG ACAGAGAGCG CGAGAGATGG AGATGGGCAG ACGGATTCAT  
 61 cggcgcggga gcctctgcag agagagagcg cgagagatgg agatgggcag acggattcat

4,477 TCAGAGCTGC GGAACAGGGC GCCCTCTGAT GTGAAAGAAC TTGCCCTGGA CAACAGTCGG  
 121 ttagagctgc ggaacaggac gccctctgat gtgaaagaac ttgtcctgga caacagtcgg

4,537 TCGAATGAAG CCAAACCTCGA AGCCCTCACA GATGAATTTG AAGAACTGGA ATTCTTAAGT  
 181 tcgaatgaag gcaaactcga aggcctcaca gatgaatttg aagaactgga attcttaagt

4,597 AAAATCAACG GAGGCCTCAC CTCAATCTCA GACTTACCAA AGTTAAAGTT GAGA---AAG  
 241 acaatcaacg taggcctcac ctcaatcgca aacttaccaa agttaaacia acttaagaag

4,654 CTTGAACTAA -----G AGTCTCAGGG GGCCTGGAAG TATTGGCAGA AAAGTGTCCTA  
 301 cttgaactaa gcgataacag agtctcaggg ggcctagaag tattggcaga aaagtgtccg

4,705 AACCTCACGC ATCTATATTT AAGTGGCAAC AAAATTAAAG ACCTCAGCAC AATAGAGCCA  
 361 aacctcacgc atctaaatth aagtggcaac aaaattaaag acctcagcac aatagagcca

4,765 CTGAAACAGT TAGAAAACCT CAAGAGCTTA GACCTTTTCA ATTGCGAGGT AACCAACCTG  
 421 ctgaaaaagt tagaaaacct caagagctta gaccttttca attgcgaggt aaccaacctg

4,825 AACGACTACG GAGAAAACGT GTTCAAGCTT CTCTTGCAAC TCACATATCT CGACAGCTGT  
 481 aacgactacc gagaaaatgt gttcaagctc ctcccgaac tcacatatct cgacaggctat

4,885 TACTGGGACC ACAAGGAGGC CCCTTACTCA GATATTGAGG ACCACGTGGA GGGCCTGGAT  
 541 gaccgggacg acaaggaggc ccctgactcg gatgttgagg gctacgtgga gggcctggat

4,945 GACGAGGAGG AGGGTGAGCA TGAGGAGGAG TATGATGAAG ATGCTCAGGT AGTGAAGAT  
 601 gatgaggagg aggatgagga tgaggaggag tatgatgaag atgctcaggt agtgaagac

5,005 GAGGAGGGCG AGGAGGAGGA GGAGGAAGGT GAAGAGGAGG ACGTGAGTGG AGGGGACGAG  
 661 gaggaggacg aggatgagga ggaggaaggt gaagaggagg acgtgagtgg agaggaggag

FIG. 3

FIG. 3 - Continued

5,065 GAGGATGAAG AAGGTTATAA CGATGGAGAG GTAGATGGCG AGGAAGATGA AGAAGAGCTT  
 721 gaggatgaag aaggttataa cgatggagag gtagatgacg aggaagatga agaagagctt

5,125 GGTGAAGAAG AAAGGGGTCA GAAGCGAAAA TGAGAACCTG AAGATGAGGC AGAAGATGAT  
 781 ggtgaagaag aaaggggtca gaagcgaaaa cgagaacctg aagatgaggg agaagatgat

5,185 GACTAAGTAG AATAACCTAT TTTGAAAAAT TCCTATTGTG ATTGACTGT TTTTACCCAT  
 841 gactaagtgg aataacctat ttgaaaaaat tcctattgtg atttgactgt ttttaccat

5,245 ATCCCCCTCC CCCTCC---- --AATCCTGC CCCCTGAAAC TTACTTTTTT CTGATTGTAA  
 901 atccccctct cccccccct ctaatcctgc cccctgaaac ttattttttt ctgattgtaa

5,299 CATTGCTGTG GGAATGAGAC GGGAAAAGTG TACTGGGGGT TGTGGAGGGA GGGAGGGCAG  
 961 cgttgctgtg ggaacgagag ggggaagagt tactgggggt tgcgggggga ggatggcggg

5,359 GAGGCGGTGG ACTAAAATAC TATTTTTACT GCC  
 1,021 tggg-ggtgg aataaaatac tatttttact gcc

1 MEMGRRIHSE LRNRAPSDVK ELALDNSRSN EGKLEALTDE  
 1 MEMGRRIHLE LRNRTPSDVK ELVLDNSRSN EGKLEGLTDE  
  
 41 FEELEFLSKI NGGLTSISDL PKL-KLRKLE L---RVSGGL  
 41 FEELEFLSTI NVGLTSIANL PKLNKLKKLE LSDNRVSGGL  
  
 77 EVLAEKCPNL THLYLSGNKI KDLSTIEPLK QLENLKSLDL  
 81 EVLAEKCPNL THLNLSGNKI KDLSTIEPLK KLENLKSLDL  
  
 117 FNCEVTNLND YCENVFKLLL QLTYLDSCYW DHKEAPYSDI  
 121 FNCEVTNLND YRENVFKLLP QLTYLDGYDR DDKEAPSDA  
  
 157 EDHVEGLDDE EEGEEHEEYD EDAQVVEDEE GEEEEEGEE  
 161 EGYVEGLDDE EEDEDEEEYD EDAQVVEDEE DEDEEEEGEE  
  
 197 EDVSCGDEED EEGYNDGEVD GEEDEEELGE EERGQKRK\*-  
 201 EDVSGEEED EEGYNDGEVD DEEDEEELGE EERGQKRKRE  
  
 -----  
 241 PEDEGEDDD\*

FIG. 4



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...  
GGGTTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCTCTGCAGACA  
GAGAGCGCGAGAGATGGAGATGGGCAGACGGATTCATTCAGAGCTGCGGAA  
CAGGGCGCCCTCTGATGTGAAAGAACTTGCCCTGGACAACAGTCGGTCGAA  
TGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCTT  
AAGTAAAATCAACGGAGGCCTCACCTCAATCTCAGACTTACCAAAGTTAAA  
GTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCCTGGAAGTATTGGCAGA  
AAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAAGA  
CCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGA  
CCTTTTCAATTGCGAGGTAACCAACCTGAACGACTACGGAGAAAACGTGTTC  
AAGCTTCTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAGG  
AGGCCCCCTTACTCAGATATTGAGGACCACGTGGAGGGCCTGGATGACGAGG  
AGGAGGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAG  
ATGAGGAGGGCGAGGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGT  
GGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGG  
CGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAA  
AATGAGAACCTGAAGATGAGGGAGAAGATGATGACTAAGTAGAATAACCTA  
TTTTGAAAAATTCCTATTGTGATTTGACTGTTTTTACCCATATCCCCTCCCC  
CTCCAATCCTGCCCCCTGAA

FIG. 5

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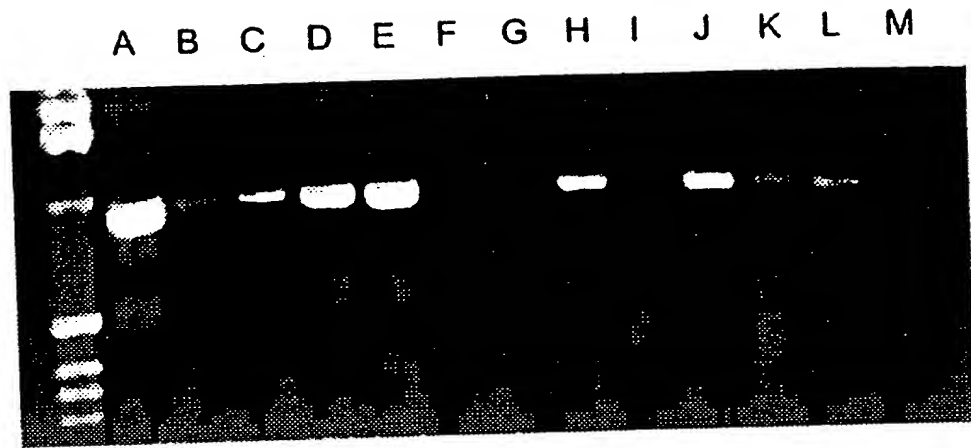
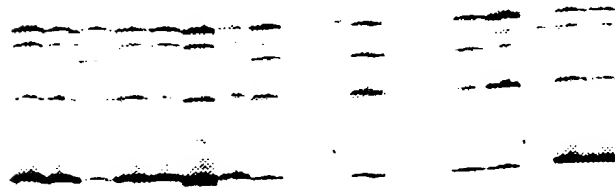


FIG. 6A

CFLP Analysis of pp32 Variants in  
Human Prostatic Adenocarcinoma

a b c d e f g h i j k l m n o p q r s



Normal pp32

Normal pp32

FIG. 6B

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	1								50
hpp32					c				
AF008216		a			g		a	a	
TSU6					g				
TSU3					g		a	a	
TSU1			g				t	a	..
P8					c				
P3			g				t	a	
L3					c				
FT3-3					g		a	a	
FT3-18			g				t	a	..
FT2-4			g				t	a	..
FT2-2					g		a	a	
FT1-7					c				
FT1-3					c				
FT1-11			g				t	a	..
D5					c				
D3					c				
D1					c				
Consensus	GGGTT	CGGGG	TTTATT	GATT	GAATT	CCGCT	GGCG	CGGGAG	CCTCTGCAGA
	51								100
hpp32									c
AF008216	c								
TSU6									c
TSU3	c				c				
TSU1		a		t			a	t	
P8									
P3		a	c	...	t		a	t	
L3									c
FT3-3	c								
FT3-18		a		t			a	t	
FT2-4		a		t			a	t	
FT2-2	c								c
FT1-7		g							
FT1-3									
FT1-11		a		t			a	t	c
D5									
D3									
D1					g				
Consensus	GAGAG	AGCGC	-GAGAG	ATGG	AGATG	GGGCAG	ACGG	ATTTCAT	TTAGAGCTGC

FIG. 7A

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FIG. 7A - Continued

	101				150
hpp32					
AF008216		g		c	
TSU6	g				
TSU3		g		c	
TSU1			c	t	a
P8					
P3			c	t	a
L3					
FT3-3		g		c	
FT3-18			c	t	a
FT2-4			c	t	a
FT2-2		g			
FT1-7					
FT1-3					
FT1-11			c	t	a
D5				t	
D3					
D1					
Consensus	GGAACAGGAC	GCCCTCTGAT	GTGAAAGAAC	TTGTCCTGGA	CAACAGTCGG
	151				200
hpp32					
AF008216			c		
TSU6					
TSU3			c		
TSU1	a	t g			
P8					
P3	a	t g			
L3					
FT3-3			c		
FT3-18	a	t g		g	
FT2-4	a	t g			
FT2-2			c		
FT1-7					
FT1-3			g		
FT1-11	a	t g			
D5					
D3					
D1					
Consensus	TCGAATGAAG	GCAAACCTCGA	AGGCCTCACA	GATGAATTTG	AAGAACTGGA

FIG. 7A - Continued

	201				250
hnp32					
AF008216		a	g	t	g
TSU6					
TSU3		a	g	t	g
TSU1	a	a	a	t	g
P8					g
P3	a	a	a	t	g
L3					
FT3-3		a	g	t	g
FT3-18	a	a	a	t	g
FT2-1	a	a	a	t	g
FT2-2		a	g	t	g
FT1-7					
FT1-3					
FT1-11	a	a	a	t	g
D5					
D3					
D1					
Consensus	ATTCTTAAGT ACAATCAACG TAGGCCTCAC CTCATCGCA AACTTACCAA				
	251				300
hnp32				ga	
AF008216	...	gt g ga	. . . . .	c	t
TSU6					
TSU3	...	gt g ga	. . . . .	c	t
TSU1				c	t
P8				c	t
P3					
L3				ga	
FT3-3	...	gt g ga	. . . . .	c	t
FT3-18				c	t
FT2-4					
FT2-2	...	gt g ga	. . . . . a		
FT1-7	...	gt g ga	. . . . .		
FT1-3			ga		
FT1-11				c	t
D5			ga		
D3			ga		
D1			ga		
Consensus	AGTTAAACAA ACTTAAGAAG CTTGAACTAA GCAGTAACAG AGTCTCAGGG				

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FIG. 7A - Continued

	301			350
hpp32		g		t
AF008216	g		ta	
TSU6				t
TSU3	g		ta	
TSU1			ta	
P8			ta	
P3			ta	
L3	g	g		t
FT3-3	g		ta	
FT3-18			ta	
FT2-4				t
FT2-2	g			c t
FT1-7	g			
FT1-3	g	g	ta	
FT1-11				
D5		g	ta	
D3				
D1	g	g		
Consensus	GGCCTAGAAG	TATTGGCAGA	AAAGTGTCCA	AACCTCACGC ATCTAAATTT
	351			400
hpp32				c
AF008216			c	
TSU6				c
TSU3			c	
TSU1				
P8			c	
P3				
L3				c
FT3-3			c	
FT3-18			c	
FT2-4				c
FT2-2				c
FT1-7				
FT1-3			c	
FT1-11				
D5			c	
D3				
D1				
Consensus	AAGTGGCAAC	AAAATTAAAG	ACCTCAGCAC	AATAGAGCCA CTGAAAAAGT

FIG. 7A - Continued

401					450
hnp32					
AF008216					
TSU6		g			c
TSU3					c
TSU1		g		c	
P8					c
P3		g			c
L3					
FT3-3					c
FT3-18		tg			c
FT2-4		g			c
FT2-2					
FT1-7					
FT1-3					c
FT1-11		g			c
D5					c
D3		g			
D1					
Consensus	TAGAAAACCT	CAAGAGCTTA	GACCTTTTCA	ATTGCGAGGT	AACCAACCTG
					500
451					
hnp32					c
AF008216		g	c	t	
TSU6	a	t	g	ga	
TSU3		g		c	t
TSU1	a	t		ga	
P8					c
P3	a				c
L3					c
FT3-3		g	c	t	
FT3-18	a	t	ga		
FT2-4	a	t	ga		
FT2-2		g	c	t	
FT1-7		g	c	t	
FT1-3					c
FT1-11	a	t	ga		c
D5					c
D3	a	t	ga		c
D1					
Consensus	AACCACTACC	GAGAAAATGT	GTTCAAGCTC	CTCCTGCAAC	TCACATATCT

FIG. 7A - Continued

	501					550
hnp32		a				
AF008216	a	a	t	t	c	t a at
TSU6	a			c	t	a g
TSU3	a		t	t	c	t a at
TSU1	a			c	t	a g
P8		a				
P3		a				
L3		a				
FT3-3	a		t	t	c	t a at
FT3-18	a			c	t	a g
FT2-4	a			c	t	a g
FT2-2	a		t	t	c	t a at
FT1-7	a		t	t	c	t a at
FT1-3		a				
FT1-11	a			c	t	a g
D5		a				
D3	a			c	t	a g
D1		a				
Consensus	CGACGGCTGT	GACCGGGACG	ACAAGGAGGC	CCCTGACTCG	GATGCTGAGG	
	551					600
hnp32				t		
AF008216	a c					g c
TSU6	tt		t	a		
TSU3	c c					g c
TSU1	tt		t	a		
P8				t		
P3				t		
L3				t		
FT3-3	a c					g c
FT3-18				c	t	
FT2-4	tt		t		a	
FT2-2	a c					g c
FT1-7	a c					g c
FT1-3				t		
FT1-11	tt		t	a		
D5				t		
D3	tt		t	a		
D1				t		
Consensus	GCTACCTGGA	GGCCTGGAT	GACGAGGAGG	AGGATGAGGA	TGAGGAGGAG	



FIG. 7A - Continued

	601			650
hnp32		c		
AF008216			g	g
TSU6	a			
TSU3			g	g
TSU1	a			
P8	a	c		
P3		c		
L3		c		
FT3-3			g	g
FT3-18		c		
FT2-4	a			
FT2-2			g	g
FT1-7			g	g g
FT1-3		c		
FT1-11	a			
D5		c		
D3	a			
D1		c		
Consensus	TATGATGAAG	ATGCTCAGGT	AGTGGAAGAT	GAGGAGGACG AGGATGAGGA
	651			700
hnp32			g c	
AF008216			c	a g t
TSU6	c		g c	
TSU3			c	a g t
TSU1	c			
P8				
P3				
L3				
FT3-3			g c g	
FT3-18				
FT2-4	c		c	a g t
FT2-2			g c	
FT1-7			g c	
FT1-3				
FT1-11	c		c	a g t
D5				
D3	c		c	a g t
D1				
Consensus	GGAGGAAGGT	GAAGAGGAGG	ACCTGAGTGG	AGAGGAGGAG GAGGATGAAG

FIG. 7A - Continued

	701			750
hpp32				
AF008216			g	
TSU6	a		t	
TSU3			g	
TSU1	a		t	
P8				
P3				
L3				
FT3-3			g	
FT3-18				
FT2-4	a		t	
FT2-2			g	
FT1-7				
FT1-3				
FT1-11	a		t	
D5				
D3	a		t	
D1				
Consensus	AAGGTTATAA	CGATGGAGAG	GTAGATGACG	AGGARGATGA AGAAGAGCTT
	751			800
hpp32			c	
AF008216			t	
TSU6			ta	a
TSU3			t	
TSU1			ta	a
P8			c	
P3			c	
L3			c	
FT3-3			t	
FT3-18			c	
FT2-4			ta	a
FT2-2			t	
FT1-7			c	
FT1-3			c	
FT1-11			ta	a
D5			c	
D3			ta	a
D1			c	
Consensus	GGTGAAGAAG	AAAGGGGTCA	GAGCGAAAA	-GAGAACCTG AAGATGAGGG

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# FIG. 7A - Continued

801					850
hnp32			a		
AF008216				t	t
TSU6	c	c			
TSU3			a		t
TSU1	c	c		t	
P8					
P3					
L3					
FT3-3			a		
FT3-18				t	t
FT2-4	c	c			
FT2-2			a		
FT1-7					
FT1-3				t	t
FT1-11	c	c			
D5				t	
D3	c	c			
D1					
Consensus	AGAAGATGAT	GACTAAGTGG	AATAACCTAT	TTTGAAAAAT	TCCTATTGTG

					900
851					
hnp32					c
AF008216				...	a
TSU6	t	g	g	c	
TSU3				...	a
TSU1	t	g	g	...	
P8					
P3					
L3					
FT3-3				a	
FT3-18		g	g	...	a
FT2-4	t	g	g	...	a
FT2-2				c...	
FT1-7					
FT1-3					a
FT1-11	t	g	g	...	
D5					
D3					
D1					
Consensus	ATTTGACTGT	TTTTACCCAT	ATCCCCTCTC	CCCCCCCCCT	CTAATCCTGC

## FIG. 7A - Continued

901

hpp32

AF008216

TSU6

TSU3

TSU1

P8

P3

L3

FT3-3

FT3-18

FT2-4

FT2-2

FT1-7

FT1-3

FT1-11

D5

D3

D1

Consensus CCCCTGAA

1

hpp32							
TSU-6		g					l n
TSU-1	kw			f	q		
PC3-8							l n
PC3-3	kw			f	q		k
FT3-3		s	a	a		a	l n
FT3-18	kw			f	q		k
FT2-2		s	a			a	
FT1-7							
DU-145-5				v			
DU-145-3							
Consensus	MEMGRRIHLE LRNRTPSDVK ELVLDNSRSN EGKLEGLTDE FEELEFLSTI						

51

hpp32				d			t
TSU-6				a v			
TSU-1	i			a v			
PC3-8				a v			
PC3-3	i			a v			
FT3-3	g	sd	.	r	...		t y
FT3-18	i				a v		
FT2-2	g	sd	.	r	...k		t y
FT1-7			.	r	...		t y
DU-145-5				d			t
DU-145-3				d			
Consensus	NVGLTSIANL PKLNKLKKLE LSSNRVSGGL EVLAEKCPNL IHLNLSGNKI						

101

hpp32							
TSU-6		e	t	n	-----	-----	
TSU-1		e	t	n	-----	-----	
PC3-8			s				
PC3-3		e	t	n			
FT3-3	q				g	l	scyw
FT3-18		e	t	n	-----	-----	
FT2-2	q				g	l	scyw
FT1-7	q				g	l	scyw
DU-145-5							
DU-145-3		e	t	n	-----	-----	
Consensus	KDLSTIEPLK KLENLKSLDL FNCEVTNLND YRENVFKLLP QLTYLDGYDR						

FIG. 7B

## FIG. 7B - Continued

	151						200
hpp32							
TSU-6	-----	-----	-----	-----	-----	-----	
TSU-1	-----	-----	-----	-----	-----	-----	
PC3-8							
PC3-3							
FT3-3	h	y	i	dh	g	h	g e
FT3-18	-----	-----	-----	-----	-----	-----	
FT2-2	h	y	i	dh	g	h	g e
FT1-7	h	y	i	dh	g	h	g eg
DU-145-5							
DU-145-3	-----	-----	-----	-----	-----	-----	
Consensus	EDKEAPSDA	EGYVEGLDDE	EEDEDEEEYD	EDAQVVEDEE	DEDEEEEGEE		
	201						249
hpp32							
TSU-6	-----	-----	-----	-----	-----	-----	
TSU-1	-----	-----	-----	-----	-----	-----	
PC3-8							
PC3-3							
FT3-3	gdg			g			
FT3-18	-----	-----	-----	-----	-----	-----	
FT2-2	gd			g			
FT1-7	gd						
DU-145-5							
DU-145-3	-----	-----	-----	-----	-----	-----	
Consensus	EDVSGEEED	EEGYNDGEVD	DEEDEEELGE	EERGQKRKRE	PEDEGEDDD		
	1						50
hpp32							
TSU-6			g				
TSU-1	kw			f	q		l n
PC3-8							
PC3-3	kw			f	q		l n
FT3-3		s	a	a		a	k
FT3-18	kw			f	q		l n
FT2-2		s	a			a	k
FT1-7							
DU-145-5				v			
DU-145-3							
Consensus	MEMGRRIHLE	LRNRTPSDVK	ELVLDNSRSN	EGKLEGLTDE	FEELEFLSTI		

## FIG. 7B - Continued

	51								100
hpp32				d				t	
TSU-6				a v					
TSU-1	i			a v					
PC3-8				a v					
PC3-3	i			a v					
FT3-3	g	sd	.	r	...			t y	
FT3-18	i				a v				
FT2-2	g	sd	.	r	...k			t y	
FT1-7			.	r	...			t y	
DU-145-5				d				t	
DU-145-3				d					
Consensus	NVGLTSIANL	PKLNKLE	LSSNRVSGGL	EVLAEKCPNL	IHLNLSGNKI				
	101								150
hpp32									
TSU-6		e	t	n	-----				
TSU-1		e	t	n	-----				
PC3-8			s						
PC3-3		e	t	n					
FT3-3	q				g	l	scyw		
FT3-18		e	t	n	-----				
FT2-2	q				g	l	scyw		
FT1-7	q				g	l	scyw		
DU-145-5									
DU-145-3		e	t	n	-----				
Consensus	KDLSTIEPLK	KLENLKS	LDL	FNCEVTNLND	YRENVFKLLP	QLTYLDGYDR			
	151								200
hpp32									
TSU-6	-----								
TSU-1	-----								
PC3-8									
PC3-3									
FT3-3	h	y	i	dh	g h		g e		
FT3-18	-----								
FT2-2	h	y	i	dh	g h		g e		
FT1-7	h	y	i	dh	g h		g eg		
DU-145-5									
DU-145-3	-----								
Consensus	DDKEAPSDA	EGYVEGLDDE	EEDEDEEEYD	EDAQVVEDEE	DEDEEEEGEE				

FIG. 7B - Continued

	201			249
hpp32				
TSU-6	-----	-----	-----	-----
TSU-1	-----	-----	-----	-----
PC3-8				
PC3-3				
FT3-3	gdg		g	-- -----
FT3-18	-----	-----	-----	-----
FT2-2	gd		g	-- -----
FT1-7	gd			
DU-145-5				
DU-145-3	-----	-----	-----	-----
Consensus	EDVSGEEEEED	EEGYNDGEVD	DEEDEEELGE	EERGQKRKRE PEDEGEDDD



pp32R1 Stimulates Transformed Focus Formation by ras + myc

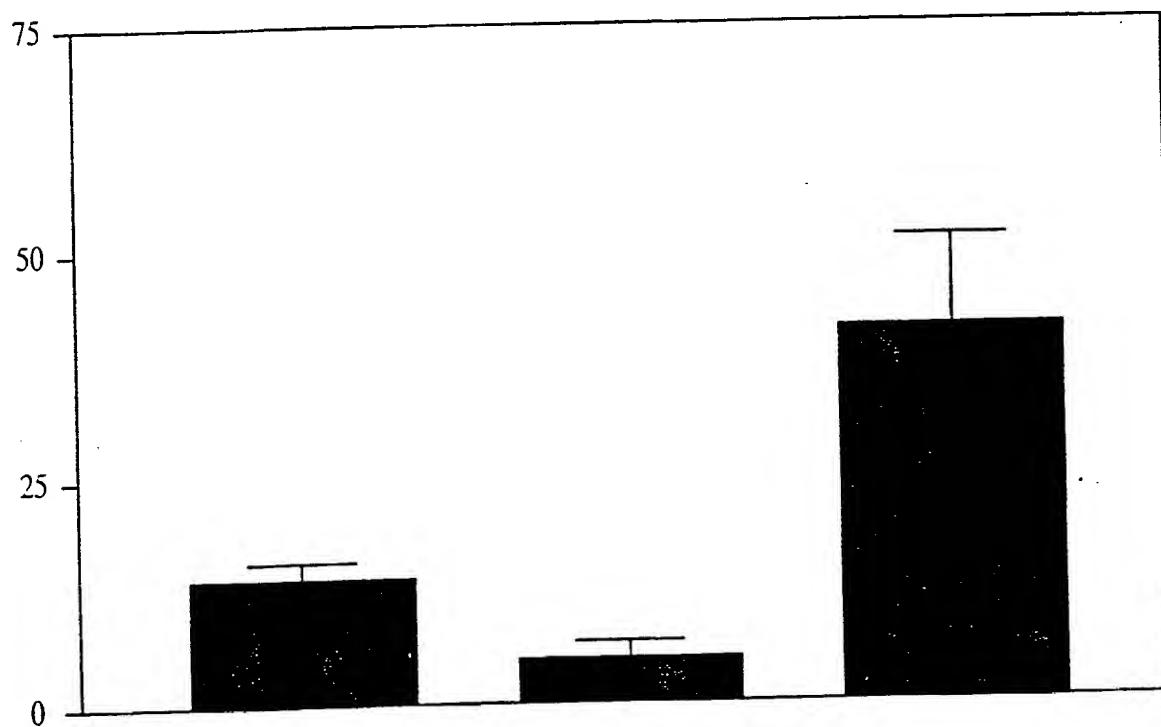


FIG. 8

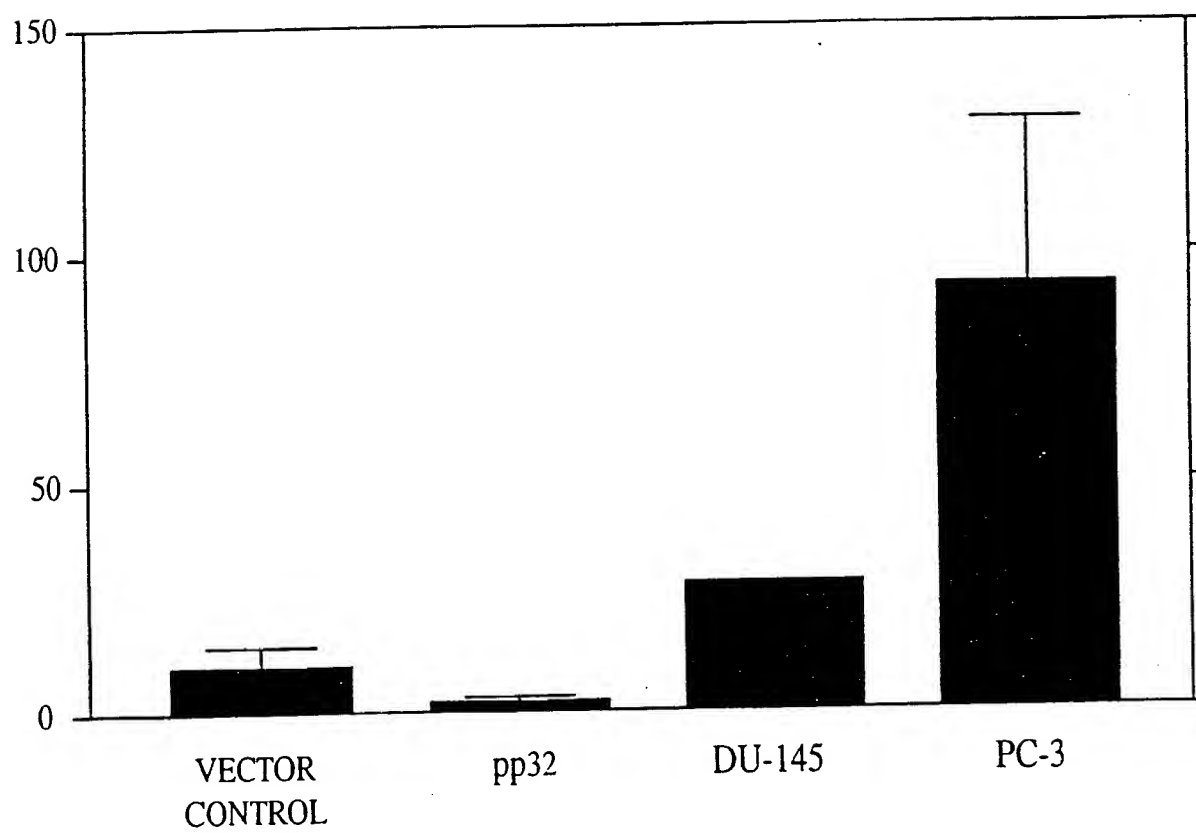


FIG. 9

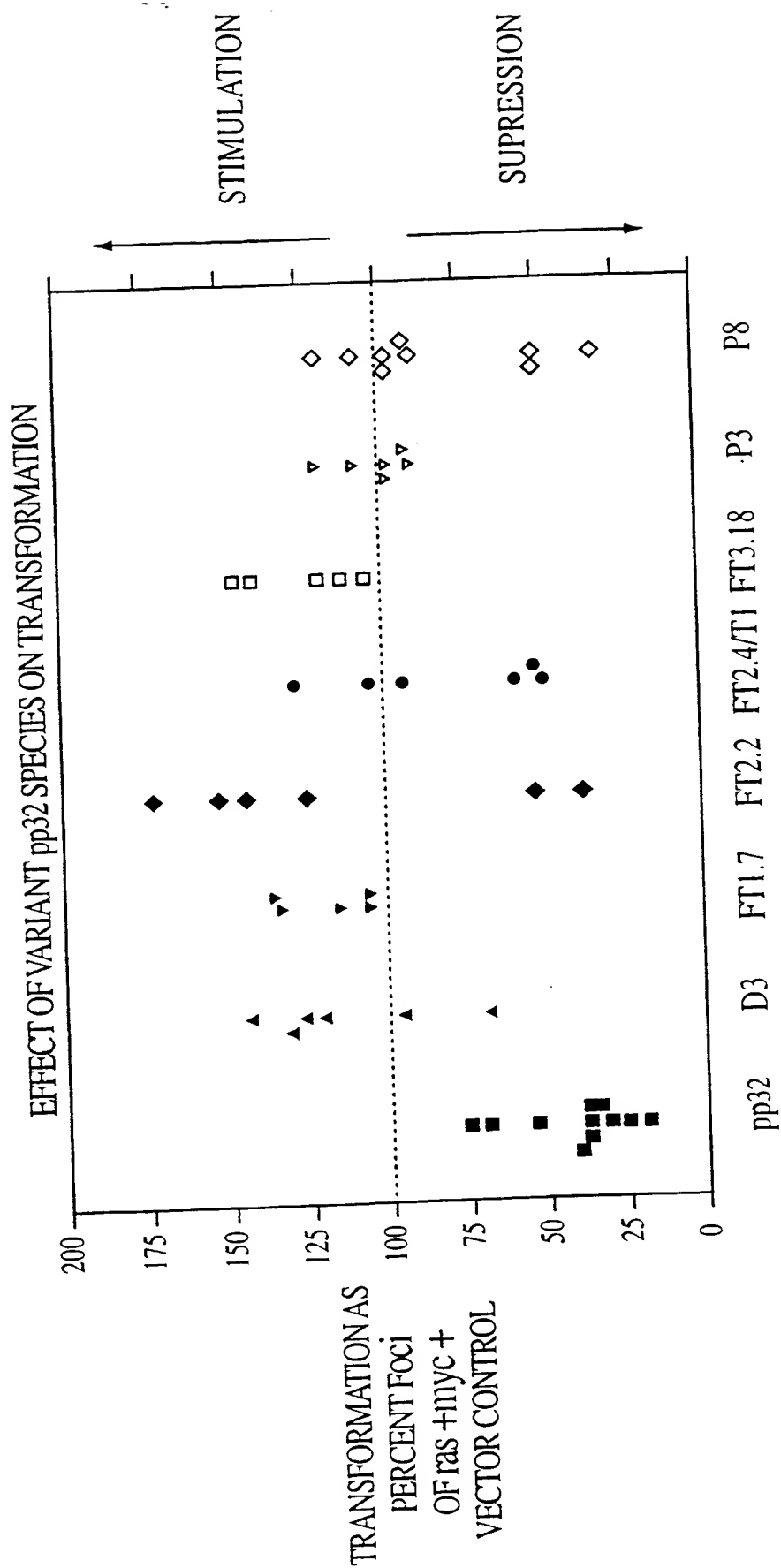


FIG. 10